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**RAW SEQUENCE LISTING**  
**ERROR REPORT**

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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,309

Source: OIPK

Date Processed by STIC: 12/6/2001

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
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OPIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:48

Input Set : A:\es.txt  
Output Set: N:\CRF3\12062001\I647309.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Pierre Fabre Medicament  
5 <120> TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY  
7 <130> FILE REFERENCE: D17064  
9 <140> CURRENT APPLICATION NUMBER: US/09/647,309  
10 <141> CURRENT FILING DATE: 2001-11-30  
12 <150> PRIOR APPLICATION NUMBER: FR 98 03814  
13 <151> PRIOR FILING DATE: 1998-03-27  
15 <160> NUMBER OF SEQ ID NOS: 136  
17 <170> SOFTWARE: PatentIn Vers. 2.0

OK

## ERRORED SEQUENCES

19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 1032  
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22 <213> ORGANISM: Klebsiella pneumoniae  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (1)..(1032)  
27 <223> OTHER INFORMATION: rP40  
29 <400> SEQUENCE: 1  
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31 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp  
32 1 5 10 15  
34 tat gca ggt ggt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc 96  
35 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe  
36 20 25 30  
38 tac ggt aac ggt ttc cag aac aac ggt ccg acc cgt aac gat cag 144  
39 Tyr Gly Asn Gly Phe Gln Asn Asn Gly Pro Thr Arg Asn Asp Gln  
40 35 40 45  
42 ctt ggt gct ggt gcg ttc ggt ggt tac cag gtt aac ccg tac ctc ggt 192  
43 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly  
44 50 55 60  
46 ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc 240  
47 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser  
48 65 70 75 80  
50 gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa 288  
51 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys  
52 85 90 95  
54 ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc 336  
55 Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly  
56 100 105 110  
58 ggc atg gtt tgg cgc gct gac tcc aaa ggc aac tac gct tct acc ggc 384  
59 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly  
60 115 120 125  
62 gtt tcc cgt agc gaa cac gac act ggc gtt tcc cca gta ttt gtc ggc 432

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:48

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Output Set: N:\CRF3\12062001\I647309.raw

63	Val	Ser	Arg	Ser	Glu	His	Asp	Thr	Gly	Val	Ser	Pro	Val	Phe	Ala	Gly	
64	130				135					140							
66	ggc	gta	gag	tgg	gct	gtt	act	cgt	gac	atc	gct	acc	cgt	ctg	gaa	tac	480
67	Gly	Val	Glu	Trp	Ala	Val	Thr	Arg	Asp	Ile	Ala	Thr	Arg	Leu	Glu	Tyr	
68	145				150					155				160			
70	cag	tgg	gtt	aac	aac	atc	ggc	gac	gct	ggc	act	gtg	ggt	acc	cgt	cct	528
71	Gln	Trp	Val	Asn	Asn	Ile	Gly	Asp	Ala	Gly	Thr	Val	Gly	Thr	Arg	Pro	
72					165					170				175			
74	gat	aac	ggc	atg	ctg	agc	ctg	ggc	gtt	tcc	tac	cgc	ttc	ggt	cag	gaa	576
75	Asp	Asn	Gly	Met	Leu	Ser	Leu	Gly	Val	Ser	Tyr	Arg	Phe	Gly	Gln	Glu	
76					180					185				190			
78	gat	gct	gca	ccg	gtt	gtt	gct	ccg	gct	ccg	gct	ccg	gaa	gtg		624	
79	Asp	Ala	Ala	Pro	Val	Val	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Glu	Val	
80		195				200					205						
82	gct	acc	aag	cac	ttc	acc	ctg	aag	tct	gac	gtt	ctg	ttc	aac	ttc	aac	672
83	Ala	Thr	Lys	His	Phe	Thr	Leu	Lys	Ser	Asp	Val	Leu	Phe	Asn	Phe	Asn	
84		210				215					220						
86	aaa	gct	acc	ctg	aaa	ccg	gaa	ggt	cag	cag	gct	ctg	qat	cag	ctg	tac	720
87	Lys	Ala	Thr	Leu	Lys	Pro	Glu	Gly	Gln	Gln	Ala	Leu	Asp	Gln	Leu	Tyr	
88	225				230					235				240			
90	act	cag	ctg	agc	aac	atg	gat	ccg	aaa	gac	ggt	tcc	gct	gtt	gtt	ctg	768
91	Thr	Gln	Leu	Ser	Asn	Met	Asp	Pro	Lys	Asp	Gly	Ser	Ala	Val	Val	Leu	
92		245				250					255						
94	ggc	tac	acc	gac	ccg	atc	ggt	tcc	gaa	gct	tac	aac	cag	cag	ctg	tct	816
95	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Ser	Glu	Ala	Tyr	Asn	Gln	Gln	Leu	Ser	
96		260				265					270						
98	gag	aaa	cgt	gct	cag	tcc	gtc	gtt	gac	tac	ctg	gtt	gct	aaa	ggc	atc	864
99	Glu	Lys	Arg	Ala	Gln	Ser	Val	Val	Asp	Tyr	Leu	Val	Ala	Lys	Gly	Ile	
100		275				280					285						
102	ccg	gct	ggc	aaa	atc	tcc	gct	ccg	ggc	atg	ggt	gaa	tcc	aac	ccg	gtt	912
103	Pro	Ala	Gly	Lys	Ile	Ser	Ala	Arg	Gly	Met	Gly	Glu	Ser	Asn	Pro	Val	
104		290				295					300						
106	act	ggc	aac	acc	tgt	gac	aac	gtg	aaa	gct	ccg	gct	gcc	ctg	atc	gat	960
107	Thr	Gly	Asn	Thr	Cys	Asp	Asn	Val	Lys	Ala	Arg	Ala	Ala	Leu	Ile	Asp	
108	305					310					315				320		
110	tgc	ctg	gct	ccg	gat	cgt	cgt	gta	gag	atc	gaa	gtt	aaa	ggc	tac	aaa	1008
111	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val	Glu	Ile	Glu	Val	Lys	Gly	Tyr	Lys	
112		325									330			335			
114	gaa	gtt	gta	act	cag	cct	cag	gct								1032	
115	Glu	Val	Val	Thr	Gln	Pro	Gln	Ala									
116		340															
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193	<211>	LENGTH:	303														
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195	<213>	ORGANISM:	Respiratory Syncytial Virus (RSV)														
197	<220>	FEATURE:															
198	<221>	NAME/KEY:	CDS														
199	<222>	LOCATION:	(1)..(303)														
201	<220>	FEATURE:															

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:48

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Output Set: N:\CRF3\12062001\I647309.raw

202 <223> OTHER INFORMATION: G2A  
 204 <400> SEQUENCE: 3  
 205 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa 48  
 206 Thr Val Lys Thr Lys Asn Thr Thr Thr Gln Thr Gln Pro Ser Lys  
 207 1 5 10 15  
 209 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac 96  
 210 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn  
 211 20 25 30  
 213 gat ttc cat ttc gaa gtg ttc aac ttc gtg ccg tgc agc atc tgc agc 144  
 214 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser  
 215 35 40 45  
 217 aac aac ccg acc tgc tgg gcg atc tgc aaa cgt atc ccg aac aaa aaa 192  
 218 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys  
 219 50 55 60  
 221 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa 240  
 222 Pro Gly Lys Lys Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys  
 223 65 70 75 80  
 225 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg 288  
 226 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val  
 227 85 90 95  
 229 ccg acc acc aaa ccg 303  
 230 Pro Thr Thr Lys Pro  
 231 100  
 262 <210> SEQ ID NO: 5  
 263 <211> LENGTH: 303

E--> 264 <212> TYPE: ADN

265 <213> ORGANISM: Respiratory Syncytial Virus (RSV)  
 267 <220> FEATURE:  
 268 <221> NAME/KEY: CDS  
 269 <222> LOCATION: (1)..(303)  
 271 <220> FEATURE:  
 272 <223> OTHER INFORMATION: G2B  
 274 <400> SEQUENCE: 5  
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 276 Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr Asn Lys  
 277 1 5 10 15  
 279 ccg agc acc aaa agc cgt agc aaa aac ccg ccg aaa aaa ccg aaa gat 96  
 280 Pro Ser Thr Lys Ser Arg Ser Lys Asn Pro Pro Lys Lys Pro Lys Asp  
 281 20 25 30  
 283 gat tac cac ttc gaa gtg ttc aac ttc gtg ccc tgc agc atc tgc ggc 144  
 284 Asp Tyr His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Gly  
 285 35 40 45  
 287 aac aac cag ctg tgc aaa agc atc tgc aaa acc atc ccg agc aac aaa 192  
 288 Asn Asn Gln Leu Cys Lys Ser Ile Cys Lys Thr Ile Pro Ser Asn Lys  
 289 50 55 60  
 291 ccg aaa aag aaa ccg acc atc aaa ccg acc aac aaa ccg acc acc aaa 240  
 292 Pro Lys Lys Lys Pro Thr Ile Lys Pro Thr Asn Lys Pro Thr Thr Lys  
 293 65 70 75 80  
 295 acc acc aac aaa cgt gat ccg aaa acc ccg gcg aaa atg ccg aag aag 288

## RAW SEQUENCE LISTING

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DATE: 12/06/2001

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Input Set : A:\es.txt

Output Set: N:\CRF3\12062001\I647309.raw

296 Thr Thr Asn Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Pro Lys Lys  
 297 85 90 95

303

299 gaa atc atc acc aac

300 Glu Ile Ile Thr Asn

301 100

332 &lt;210&gt; SEQ ID NO: 7

333 &lt;211&gt; LENGTH: 303

E--&gt; 334 &lt;212&gt; TYPE: ADN

335 &lt;213&gt; ORGANISM: Respiratory Syncytial Virus (RSV)

337 &lt;220&gt; FEATURE:

338 &lt;221&gt; NAME/KEY: CDS

339 &lt;222&gt; LOCATION: (1)..(303)

341 &lt;220&gt; FEATURE:

342 &lt;223&gt; OTHER INFORMATION: G2AdCys

345 &lt;400&gt; SEQUENCE: 7

346 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa 48

347 Thr Val Lys Thr Lys Asn Thr Thr Thr Gln Thr Gln Pro Ser Lys

348 1 5 10 15

350 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac 96

351 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn

352 20 25 30

354 gat ttc cat ttc gaa gtg ttc aac ttc gtg ccg agc agc atc tgc agc 144

355 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Ser Ser Ile Cys Ser

356 35 40 45

358 aac aac ccg acc tgc tgg gcg atc agc aaa cgt atc ccg aac aaa aaa 192

359 Asn Asn Pro Thr Cys Trp Ala Ile Ser Lys Arg Ile Pro Asn Lys Lys

360 50 55 60

362 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa 240

363 Pro Gly Lys Lys Thr Thr Lys Pro Thr Lys Pro Thr Phe Lys

364 65 70 75 80

366 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg 288

367 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val

368 85 90 95

370 ccg acc acc aaa ccg 303

371 Pro Thr Thr Lys Pro

372 100

403 &lt;210&gt; SEQ ID NO: 9

404 &lt;211&gt; LENGTH: 303

E--&gt; 405 &lt;212&gt; TYPE: ADN

406 &lt;213&gt; ORGANISM: Respiratory Syncytial Virus (RSV)

408 &lt;220&gt; FEATURE:

409 &lt;221&gt; NAME/KEY: CDS

410 &lt;222&gt; LOCATION: (1)..(303)

412 &lt;220&gt; FEATURE:

413 &lt;223&gt; OTHER INFORMATION: G2BdCys

416 &lt;400&gt; SEQUENCE: 9

417 acc gcg cag acc aaa ggc cgt atc acc acc agc acc cag acc aac aaa 48

418 Thr Ala Gln Thr Lys Gly Arg Ile Thr Thr Ser Thr Gln Thr Asn Lys

419 1 5 10 15

## RAW SEQUENCE LISTING

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Input Set : A:\es.txt

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421	ccg	agc	acc	aaa	agc	cgt	agc	aaa	aac	ccg	ccg	aaa	aaa	ccg	aaa	gat	96	
422	Pro	Ser	Thr	Lys	Ser	Arg	Ser	Lys	Asn	Pro	Pro	Lys	Lys	Pro	Lys	Asp		
423				20					25						30			
425	gat	tac	cac	ttc	gaa	gtg	ttc	aac	ttc	gtg	ccc	agc	agc	atc	tgc	ggc	144	
426	Asp	Tyr	His	Phe	Glu	Val	Phe	Asn	Phe	Val	Pro	Ser	Ser	Ile	Cys	Gly		
427				35					40					45				
429	aac	aac	cag	ctg	tgc	aaa	agc	atc	agc	aaa	acc	atc	ccg	agc	aac	aaa	192	
430	Asn	Asn	Gln	Leu	Cys	Lys	Ser	Ile	Ser	Lys	Thr	Ile	Pro	Ser	Asn	Lys		
431				50					55			60						
433	ccg	aaa	aag	aaa	ccg	acc	aaa	ccg	acc	aaa	ccg	acc	acc	aaa		240		
434	Pro	Lys	Lys	Lys	Pro	Thr	Ile	Lys	Pro	Thr	Asn	Lys	Pro	Thr	Thr	Lys		
435	65				70					75				80				
437	acc	acc	aac	aaa	cgt	gat	ccg	aaa	acc	ccg	gcg	aaa	atg	ccg	aag	aag	288	
438	Thr	Thr	Asn	Lys	Arg	Asp	Pro	Lys	Thr	Pro	Ala	Lys	Met	Pro	Lys	Lys		
439					85					90				95				
441	gaa	atc	atc	acc	acc	aac										303		
442	Glu	Ile	Ile	Thr	Asn													
443				100														
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475	<211>	LENGTH:	42															

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484	<223>	OTHER INFORMATION:	G1ACys															
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489	Ser	Ile	Cys	Ser	Asn	Asn	Pro	Thr	Cys	Trp	Ala	Ile	Cys	Lys				
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E--&gt; 505 &lt;212&gt; TYPE: ADN

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510	<222>	LOCATION:	(1)..(42)															
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E--&gt; 535 &lt;212&gt; TYPE: ADN

536	<213>	ORGANISM:	Respiratory Syncytial Virus (RSV)															
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RAW SEQUENCE LISTING  
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539 <221> NAME/KEY: CDS  
 540 <222> LOCATION: (1)..(42)  
 542 <220> FEATURE:  
 543 <223> OTHER INFORMATION: G1A  
 546 <400> SEQUENCE: 15  
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 548 Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Ser Lys  
 549 1 5 10  
 562 <210> SEQ ID NO: 17  
 563 <211> LENGTH: 42  
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 565 <213> ORGANISM: Respiratory Syncytial Virus (RSV)  
 567 <220> FEATURE:  
 568 <221> NAME/KEY: CDS  
 569 <222> LOCATION: (1)..(42)  
 571 <220> FEATURE:  
 572 <223> OTHER INFORMATION: G1B  
 575 <400> SEQUENCE: 17  
 576 agc atc tgc ggc aac aac cag ctg tgc aaa agc atc agc aaa 42  
 577 Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Ser Lys  
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 660 <211> LENGTH: 303  
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 664 <220> FEATURE:  
 665 <221> NAME/KEY: CDS  
 666 <222> LOCATION: (1)..(303)  
 668 <220> FEATURE:  
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 675 1 5 10 15  
 677 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac 96  
 678 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn  
 679 20 25 30  
 681 gat tcc cat tcc gaa gtg tcc aac tcc gtg ccg agc agc atc tgc agc 144  
 682 Asp Ser His Ser Glu Val Ser Asn Ser Val Pro Ser Ser Ile Cys Ser  
 683 35 40 45  
 685 aac aac ccg acc tgc tgg gcg atc agc aaa cgt atc ccg aac aaa aaa 192  
 686 Asn Asn Pro Thr Cys Trp Ala Ile Ser Lys Arg Ile Pro Asn Lys Lys  
 687 50 55 60  
 689 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa ccg acc ttc aaa 240  
 690 Pro Gly Lys Lys Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys  
 691 65 70 75 80  
 693 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg 288  
 694 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val  
 695 85 90 95

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Output Set: N:\CRF3\12062001\I647309.raw

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698 Pro Thr Thr Lys Pro	
699 100	
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736 <221> NAME/KEY: CDS	
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739 <220> FEATURE:	
740 <223> OTHER INFORMATION: G4A	
742 <400> SEQUENCE: 25	
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747 aaa	51
748 Lys	
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770 <221> NAME/KEY: CDS	
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773 <220> FEATURE:	
774 <223> OTHER INFORMATION: G4AdC	
777 <400> SEQUENCE: 27	
778 gtg ccg agc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc agc 48	
779 Val Pro Ser Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Ser	
780 1 5 10 15	
782 aaa	51
783 Lys	
799 <210> SEQ ID NO: 29	
800 <211> LENGTH: 51	
<b>E--&gt; 801 &lt;212&gt; TYPE: ADN</b>	
802 <213> ORGANISM: Respiratory Syncytial Virus (RSV)	
804 <220> FEATURE:	
805 <221> NAME/KEY: CDS	
806 <222> LOCATION: (1)..(51)	
808 <220> FEATURE:	
809 <223> OTHER INFORMATION: G4B	
812 <400> SEQUENCE: 29	
813 gtg ccc tgc agc atc tgc ggc aac aac cag ctg tgc aaa agc atc tgc 48	
814 Val Pro Cys Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Cys	
815 1 5 10 15	
817 aaa	51
818 Lys	
834 <210> SEQ ID NO: 31	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:48

Input Set : A:\es.txt  
Output Set: N:\CRF3\12062001\I647309.raw

835 <211> LENGTH: 51  
**E--> 836 <212> TYPE: ADN**  
 837 <213> ORGANISM: Respiratory syncytial Virus (RSV)  
 839 <220> FEATURE:  
 840 <221> NAME/KEY: CDS  
 841 <222> LOCATION: (1)..(51)  
 843 <220> FEATURE:  
 844 <223> OTHER INFORMATION: G4BdC  
 847 <400> SEQUENCE: 31  
 848 gtg ccc agc agc atc tgc ggc aac aac cag ctg tgc aaa agc atc agc 48  
 849 Val Pro Ser Ser Ile Cys Gly Asn Asn Gln Leu Cys Lys Ser Ile Ser  
 850 1 5 10 15  
 852 aaa 51  
 853 Lys  
 949 <210> SEQ ID NO: 37  
 950 <211> LENGTH: 183  
**E--> 951 <212> TYPE: ADN**  
 952 <213> ORGANISM: Respiratory syncytial Virus (RSV)  
 954 <220> FEATURE:  
 955 <221> NAME/KEY: CDS  
 956 <222> LOCATION: (1)..(183)  
 958 <220> FEATURE:  
 959 <223> OTHER INFORMATION: G200A  
 962 <400> SEQUENCE: 37  
 963 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg 48  
 964 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro  
 965 1 5 10 15  
 967 ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg 96  
 968 Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val  
 969 20 25 30  
 971 ccg tgc agc atc tgc agc aac ccg acc tgc tgg gcg atc tgc aaa 144  
 972 Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys  
 973 35 40 45  
 975 cgt atc ccg aac aaa aaa ccg ggc aaa aaa acc acg acc 183  
 976 Arg Ile Pro Asn Lys Lys Pro Gly Lys Lys Thr Thr Thr  
 977 50 55 60  
 999 <210> SEQ ID NO: 39  
 1000 <211> LENGTH: 177  
**E--> 1001 <212> TYPE: ADN**  
 1002 <213> ORGANISM: Respiratory syncytial Virus (RSV)  
 1004 <220> FEATURE:  
 1005 <221> NAME/KEY: CDS  
 1006 <222> LOCATION: (1)..(177)  
 1008 <220> FEATURE:  
 1009 <223> OTHER INFORMATION: G198A  
 1012 <400> SEQUENCE: 39  
 1013 cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg 48  
 1014 Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro  
 1015 1 5 10 15

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:48

Input Set : A:\es.txt  
Output Set: N:\CRF3\12062001\I647309.raw

1017	ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg	96
1018	Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val	
1019	20 25 30	
1021	ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa	144
1022	Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys	
1023	35 40 45	
1025	cgt atc ccg aac aaa aaa ccg ggc aaa aaa acc	177
1026	Arg Ile Pro Asn Lys Lys Pro Gly Lys Lys Thr	
1027	50 55	
1049	<210> SEQ ID NO: 41	
1050	<211> LENGTH: 171	
E-->	1051 <212> TYPE: ADN	
1052	<213> ORGANISM: Respiratory syncytial Virus (RSV)	
1054	<220> FEATURE:	
1055	<221> NAME/KEY: CDS	
1056	<222> LOCATION: (1)..(171)	
1058	<220> FEATURE:	
1059	<223> OTHER INFORMATION: G196A	
1062	<400> SEQUENCE: 41	
1063	ccg acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg	48
1064	Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro	
1065	1 5 10 15	
1067	ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg	96
1068	Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val	
1069	20 25 30	
1071	ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa	144
1072	Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys	
1073	35 40 45	
1075	cgt atc ccg aac aaa aaa ccg ggc aaa	171
1076	Arg Ile Pro Asn Lys Lys Pro Gly Lys	
1077	50 55	
1099	<210> SEQ ID NO: 43	
1100	<211> LENGTH: 165	
E-->	1101 <212> TYPE: ADN	
1102	<213> ORGANISM: Respiratory syncytial Virus (RSV)	
1104	<220> FEATURE:	
1105	<221> NAME/KEY: CDS	
1106	<222> LOCATION: (1)..(165)	
1108	<220> FEATURE:	
1109	<223> OTHER INFORMATION: G194A	
1112	<400> SEQUENCE: 43	
1113	ccg acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg	48
1114	Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro	
1115	1 5 10 15	
1117	ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg	96
1118	Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val	
1119	20 25 30	
1121	ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa	144
1122	Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys	

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:48

Input Set : A:\es.txt  
Output Set: N:\CRF3\12062001\I647309.raw

1123	35	40	45	
1125	cgt atc ccg aac aaa aaa ccg			165
1126	Arg Ile Pro Asn Lys Lys Pro			
1127	50	55		
1149	<210> SEQ ID NO: 45			
1150	<211> LENGTH: 159			
E-->	1151 <212> TYPE: ADN			
1152	<213> ORGANISM: Respiratory syncytial Virus (RSV)			
1154	<220> FEATURE:			
1155	<221> NAME/KEY: CDS			
1156	<222> LOCATION: (1)..(159)			
1158	<220> FEATURE:			
1159	<223> OTHER INFORMATION: G192A			
1162	<400> SEQUENCE: 45			
1163	cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg	48		
1164	Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro			
1165	1 5 10 15			
1167	ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg	96		
1168	Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val			
1169	20 25 30			
1171	ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa	144		
1172	Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys			
1173	35 40 45			
1175	cgt atc ccg aac aaa	159		
1176	Arg Ile Pro Asn Lys			
1177	50			
1199	<210> SEQ ID NO: 47			
1200	<211> LENGTH: 153			
E-->	1201 <212> TYPE: ADN			
1202	<213> ORGANISM: Respiratory syncytial Virus (RSV)			
1204	<220> FEATURE:			
1205	<221> NAME/KEY: CDS			
1206	<222> LOCATION: (1)..(153)			
1208	<220> FEATURE:			
1209	<223> OTHER INFORMATION: G6A			
1212	<400> SEQUENCE: 47			
1213	cag acc cag ccg agc aaa ccg acc acc aaa cag cgt cag aac aaa ccg	48		
1214	Gln Thr Gln Pro Ser Lys Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro			
1215	1 5 10 15			
1217	ccg aac aaa ccg aac aac gat ttc cat ttc gaa gtg ttc aac ttc gtg	96		
1218	Pro Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val			
1219	20 25 30			
1221	ccg tgc agc atc tgc agc aac aac ccg acc tgc tgg gcg atc tgc aaa	144		
1222	Pro Cys Ser Ile Cys Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys			
1223	35 40 45			
1225	cgt atc ccg	153		
1226	Arg Ile Pro			
1227	50			
3327	<210> SEQ ID NO: 136			

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001

TIME: 11:26:49

Input Set : A:\es.txt

Output Set: N:\CRF3\12062001\I647309.raw

3328 &lt;211&gt; LENGTH: 15

3329 &lt;212&gt; TYPE: PRT

3330 &lt;213&gt; ORGANISM: Respiratory syncytial Virus (RSV)

3332 &lt;220&gt; FEATURE:

3333 &lt;223&gt; OTHER INFORMATION: Xaa means orn.

3335 &lt;220&gt; FEATURE:

3336 &lt;223&gt; OTHER INFORMATION: G1'

3339 &lt;400&gt; SEQUENCE: 136

Qs  
W-> 3340 Ser Ile Asp Ser Asn Asn Pro Thr Xaa Trp Ala Ile Ser Lys Cys

3341 1 5 10 15

E--&gt; 3345 I

E--&gt; 3348 -16-

E--&gt; 3349 PF82PCTSEQ/dln

delete

see next page

<210> 79  
<211> 183  
<212> ADN  
<213> Respiratory syncytial Virus (RSV)

<220>  
<221> CDS  
<222> (1)...(183)

<220> G200BdC move down - <220> never has a response  
<223> ↓

*FYI* Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:50

Input Set : A:\es.txt  
Output Set: N:\CRF3\12062001\I647309.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:194 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:264 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:334 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:405 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:476 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:505 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:535 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:564 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:621 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20  
L:621 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:638 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21  
L:638 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:655 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22  
L:655 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:661 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:732 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:766 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:801 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:836 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:882 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33  
L:882 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33  
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:902 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34  
L:902 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34  
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:922 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35  
L:922 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35  
L:922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:942 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36  
L:942 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36  
L:942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:951 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1001 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1051 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1101 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1151 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1201 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1251 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1293 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/647,309

DATE: 12/06/2001  
TIME: 11:26:50

Input Set : A:\es.txt  
Output Set: N:\CRF3\12062001\I647309.raw

L:1342 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1392 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1442 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1491 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1541 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1591 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1633 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1683 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1733 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1783 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1833 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1883 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1933 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1975 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:1982 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:2025 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2075 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2125 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2175 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2225 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2275 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2325 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2367 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2438 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2509 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2559 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2609 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2659 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:2709 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:3224 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:129  
L:3224 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:129  
L:3224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129  
L:3244 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:130  
L:3244 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:130  
L:3244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130  
L:3323 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:135  
L:3323 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:135  
L:3323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135  
L:3340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:136  
L:3340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:136  
L:3340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136  
L:3345 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:136  
M:332 Repeated in SeqNo=136  
L:3349 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:3349 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:3349 M:252 E: No. of Seq. differs, <211> LENGTH: Input:15 Found:16 SEQ:136